

# SEQUENCE LISTING

<110> FREY, Perry A.  
RUZICKA, Frank J.

<120> DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE

<130> 032026/0476

<140> US 09/330,611

<141> 1999-06-11

<150> US 09/198,942

<151> 1998-11-24

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<170> PatentIn Ver. 2.0

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Gln Arg Ile Thr Pro Glu Leu Val Asn Met Leu Lys Lys Tyr His Pro  
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180 185 190	
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Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu	
195 200 205	
cct cag cgt ata acg cct caa ttg gtg gat atg ctc aaa aaa tat cat	672
Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His	
210 215 220	
ccg gtg tgg ctg aac act cac ttc aac cac ccg aat gaa gtt acc gaa	720
Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu	
225 230 235 240	
gaa gca gta gag gct tgt gaa aga atg gcc aat gcc ggt att ccg ttg	768
Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu	
245 250 255	

ggt aac caa acg gtt tta ttg cgt gga atc aat gat tgt aca cat gtg 816  
 Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val  
 260 265 270  
 atg aag aga ttg gta cat ttg ctg gta aag atg cgt gtg cgt cct tac 864  
 Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr  
 275 280 285  
 tat ata tat gta tgc gat ctt tcg ctt gga ata ggt cat ttc cgc acg 912  
 Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr  
 290 295 300  
 ccg gta tct aaa gga atc gaa att atc gaa aat ttg cgc gga cac acc 960  
 Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr  
 305 310 315 320  
 tcg ggc tat gct gtt cct acc ttt gtg gta gat gct ccg ggg ggt ggt 1008  
 Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly  
 325 330 335  
 ggt aag ata cct gta atg ccg aac tat gtt gta tct cag tcc cca cga 1056  
 Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg  
 340 345 350  
 cat gtg gtt ctt cgc aat tat gaa ggt gtt atc aca acc tat acg gag 1104  
 His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu  
 355 360 365  
 ccg gag aat tat cat gag gag tgt gat tgt gag gac tgt cga gcc ggt 1152  
 Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly  
 370 375 380  
 aag cat aaa gag ggt gta gct gca ctt tcc gga ggt cag cag ttg gct 1200  
 Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala  
 385 390 395 400  
 atc gag cct tcc gac tta gct cgc aaa aaa cgc aag ttt gat aag aac 1248  
 Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn  
 405 410 415  
 tga 1251

<210> 8

<211> 416

<212> PRT

<213> Porphyromonas gingivalis

<400> 8

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 Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly  
 35 40 45  
 Val Lys Glu Ser Leu Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr  
 50 55 60  
 Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln  
 65 70 75 80

Ala Ile Pro Thr His Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val  
 85 90 95  
 Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His  
 100 105 110  
 Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met  
 115 120 125  
 Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala  
 130 135 140  
 Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn  
 145 150 155 160  
 Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu  
 165 170 175  
 Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile  
 180 185 190  
 Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu  
 195 200 205  
 Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His  
 210 215 220  
 Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu  
 225 230 235 240  
 Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu  
 245 250 255  
 Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val  
 260 265 270  
 Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr  
 275 280 285  
 Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr  
 290 295 300  
 Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr  
 305 310 315 320  
 Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly  
 325 330 335  
 Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg  
 340 345 350  
 His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu  
 355 360 365  
 Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly  
 370 375 380  
 Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala  
 385 390 395 400  
 Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn  
 405 410 415

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 <211> 1416  
 <212> DNA  
 <213> Bacillus subtilis

<220>  
 <221> CDS  
 <222> (1)..(1413)

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 tta tgg aag gac gtt ccg gaa gag aaa tgg aac gat tgg ctt tgg cag 96  
 Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln  
 20 25 30  
 ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat 144  
 Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
 35 40 45  
 ctg acc gag gat gaa gag gaa ggc gtc aga att tct acc aaa acg atc 192  
 Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
 50 55 60  
 ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat 240  
 Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn  
 65 70 75 80  
 ccg aga tgc ccg gta cgc atg cag tct gtg ccg ctt tct gaa gaa atg 288  
 Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met  
 85 90 95  
 cac aaa aca aaa tac gat ctg gaa gac ccg ctt cat gag gat gaa gat 336  
 His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp  
 100 105 110  
 tca ccg gta ccc ggt ctg aca cac cgc tat ccc gac cgt gtg ctg ttt 384  
 Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe  
 115 120 125  
 ctt gtc acg aat caa tgt tcc atg tac tgc cgc tac tgc aca aga agg 432  
 Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg  
 130 135 140  
 cgc ttt tcc gga caa atc gga atg ggc gtc ccc aaa aaa cag ctt gat 480  
 Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp  
 145 150 155 160  
 gct gca att gct tat atc ccg gaa aca ccc gaa atc cgc gat tgt tta 528  
 Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu  
 165 170 175  
 att tca ggc ggt gat ggg ctg ctc atc aac gac caa att tta gaa tat 576  
 Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr  
 180 185 190  
 att tta aaa gag ctg cgc agc att ccg cat ctg gaa gtc atc aga atc 624  
 Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile  
 195 200 205

gga aca aga gct ccc gtc gtc ttt ccg cag cgc att acc gat cat ctg	672
Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu	
210 215 220	
tgc gag ata ttg aaa aaa tat cat ccg gtc tgg ctg aac acc cat ttt	720
Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe	
225 230 235 240	
aac aca agc atc gaa atg aca gaa gaa tcc gtt gag gca tgt gaa aag	768
Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys	
245 250 255	
ctg gtg aac gcg gga gtg ccg gtc gga aat cag gct gtc gta tta gca	816
Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala	
260 265 270	
ggt att aat gat tgc gtt cca att atg aaa aag ctc atg cat gac ttg	864
Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu	
275 280 285	
gta aaa atc aga gtc cgt cct tat tat att tac caa tgt gat ctg tca	912
Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser	
290 295 300	
gaa gga ata ggg cat ttc aga gct cct gtt tcc aaa ggt ttg gag atc	960
Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile	
305 310 315 320	
att gaa ggg ctg aga ggt cat acc tca ggc tat gcg gtt cct acc ttt	1008
Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe	
325 330 335	
gtc gtt gac gca cca ggc gga gga ggt aaa atc gcc ctg cag cca aac	1056
Val Val Asp Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn	
340 345 350	
tat gtc ctg tca caa agt cct gac aaa gtg atc tta aga aat ttt gaa	1104
Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu	
355 360 365	
ggt gtg att acg tca tat ccg gaa cca gag aat tat atc ccc aat cag	1152
Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln	
370 375 380	
gca gac gcc tat ttt gag tcc gtt ttc cct gaa acc gct gac aaa aag	1200
Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys	
385 390 395 400	
gag ccg atc ggg ctg agt gcc att ttt gct gac aaa gaa gtt tgc ttt	1248
Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe	
405 410 415	
aca cct gaa aat gta gac aga atc aaa agg aga gag gca tac atc gca	1296
Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala	
420 425 430	
aat ccg gag cat gaa aca tta aaa gat cgg cgt gag aaa aga gat cag	1344
Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln	
435 440 445	
ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act	1392
Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr	
450 455 460	

gaa tgc gga ggg gat tct tca tga  
 Glu Cys Gly Gly Asp Ser Ser  
 465 470

1416

<210> 10  
 <211> 471  
 <212> PRT  
 <213> Bacillus subtilis

<400> 10

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Leu	Trp	Lys	Asp	Val	Pro	Glu	Glu	Lys	Trp	Asn	Asp	Trp	Leu	Trp	Gln
			20					25					30		
Leu	Thr	His	Thr	Val	Arg	Thr	Leu	Asp	Asp	Leu	Lys	Lys	Val	Ile	Asn
		35					40					45			
Leu	Thr	Glu	Asp	Glu	Glu	Glu	Gly	Val	Arg	Ile	Ser	Thr	Lys	Thr	Ile
		50				55					60				
Pro	Leu	Asn	Ile	Thr	Pro	Tyr	Tyr	Ala	Ser	Leu	Met	Asp	Pro	Asp	Asn
65				70						75					80
Pro	Arg	Cys	Pro	Val	Arg	Met	Gln	Ser	Val	Pro	Leu	Ser	Glu	Glu	Met
				85					90						95
His	Lys	Thr	Lys	Tyr	Asp	Leu	Glu	Asp	Pro	Leu	His	Glu	Asp	Glu	Asp
			100					105					110		
Ser	Pro	Val	Pro	Gly	Leu	Thr	His	Arg	Tyr	Pro	Asp	Arg	Val	Leu	Phe
		115					120					125			
Leu	Val	Thr	Asn	Gln	Cys	Ser	Met	Tyr	Cys	Arg	Tyr	Cys	Thr	Arg	Arg
	130					135					140				
Arg	Phe	Ser	Gly	Gln	Ile	Gly	Met	Gly	Val	Pro	Lys	Lys	Gln	Leu	Asp
145					150					155					160
Ala	Ala	Ile	Ala	Tyr	Ile	Arg	Glu	Thr	Pro	Glu	Ile	Arg	Asp	Cys	Leu
				165					170					175	
Ile	Ser	Gly	Gly	Asp	Gly	Leu	Leu	Ile	Asn	Asp	Gln	Ile	Leu	Glu	Tyr
			180					185					190		
Ile	Leu	Lys	Glu	Leu	Arg	Ser	Ile	Pro	His	Leu	Glu	Val	Ile	Arg	Ile
		195					200					205			
Gly	Thr	Arg	Ala	Pro	Val	Val	Phe	Pro	Gln	Arg	Ile	Thr	Asp	His	Leu
	210					215						220			
Cys	Glu	Ile	Leu	Lys	Lys	Tyr	His	Pro	Val	Trp	Leu	Asn	Thr	His	Phe
225					230					235					240
Asn	Thr	Ser	Ile	Glu	Met	Thr	Glu	Glu	Ser	Val	Glu	Ala	Cys	Glu	Lys
				245					250					255	
Leu	Val	Asn	Ala	Gly	Val	Pro	Val	Gly	Asn	Gln	Ala	Val	Val	Leu	Ala
			260					265					270		
Gly	Ile	Asn	Asp	Ser	Val	Pro	Ile	Met	Lys	Lys	Leu	Met	His	Asp	Leu
		275					280					285			

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser  
 290 295 300  
 Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile  
 305 310 315 320  
 Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe  
 325 330 335  
 Val Val Asp Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn  
 340 345 350  
 Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu  
 355 360 365  
 Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln  
 370 375 380  
 Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys  
 385 390 395 400  
 Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe  
 405 410 415  
 Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala  
 420 425 430  
 Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln  
 435 440 445  
 Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr  
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 Glu Cys Gly Gly Asp Ser Ser  
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<210> 11  
 <211> 1188  
 <212> DNA  
 <213> *Deinococcus radiodurans*

<220>  
 <221> CDS  
 <222> (1)..(1188)

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 Trp Gln Gly Val Pro Asp Glu Gln Trp Tyr Asp Trp Lys Trp Gln Leu  
 1 5 10 15  
 aag aac cgc atc aac agt gtg gag gag ttg cag gaa gtc ctg acc ctc 96  
 Lys Asn Arg Ile Asn Ser Val Glu Glu Leu Gln Glu Val Leu Thr Leu  
 20 25 30  
 acc gag tcc gag tac cgg ggt gcg tcc gcc gag ggc att ttc cgc ctc 144  
 Thr Glu Ser Glu Tyr Arg Gly Ala Ser Ala Glu Gly Ile Phe Arg Leu  
 35 40 45  
 gac atc acg ccg tat ttc gcg tcc ctc atg gac ccc gaa gac ccc acc 192  
 Asp Ile Thr Pro Tyr Phe Ala Ser Leu Met Asp Pro Glu Asp Pro Thr  
 50 55 60



tgc ccg gtg cgc cgt cag gtg att ccc acc gag gag gag ctc cag ccg	240
Cys Pro Val Arg Arg Gln Val Ile Pro Thr Glu Glu Glu Leu Gln Pro	
65 70 75 80	
ttc acc tcc atg atg gaa gac tct ctc gcg gag gat aag cac tcg ccc	288
Phe Thr Ser Met Met Glu Asp Ser Leu Ala Glu Asp Lys His Ser Pro	
85 90 95	
gtg ccg ggg ctg gtg cac cgc tac ccc gac cgc gtg ctg atg ctg gtc	336
Val Pro Gly Leu Val His Arg Tyr Pro Asp Arg Val Leu Met Leu Val	
100 105 110	
acg acc cag tgc gcg agc tac tgc cgc tac tgc acc cga agc cgc atc	384
Thr Thr Gln Cys Ala Ser Tyr Cys Arg Tyr Cys Thr Arg Ser Arg Ile	
115 120 125	
gtg ggc gac ccc acc gag acg ttc aat ccc gcc gag tat gag gcg cag	432
Val Gly Asp Pro Thr Glu Thr Phe Asn Pro Ala Glu Tyr Glu Ala Gln	
130 135 140	
ctc aac tac ctg cgc aac acc ccg cag gtg cgc gac gtg ctg ctt tcc	480
Leu Asn Tyr Leu Arg Asn Thr Pro Gln Val Arg Asp Val Leu Leu Ser	
145 150 155 160	
ggc ggc gac ccg ctc aca ctc gcg ccg aag gtg ctg ggg cgc ctg ctt	528
Gly Gly Asp Pro Leu Thr Leu Ala Pro Lys Val Leu Gly Arg Leu Leu	
165 170 175	
tcc gaa ctt cgt aaa atc gag cac atc gaa atc atc cgc atc ggc acc	576
Ser Glu Leu Arg Lys Ile Glu His Ile Glu Ile Ile Arg Ile Gly Thr	
180 185 190	
cgc gtg ccc gtg ttc atg ccc atg cgc gtg acc cag gaa ctg tgc gac	624
Arg Val Pro Val Phe Met Pro Met Arg Val Thr Gln Glu Leu Cys Asp	
195 200 205	
acg ctc gcc gaa cac cat ccg ctg tgg atg aac att cac gtc aac cac	672
Thr Leu Ala Glu His His Pro Leu Trp Met Asn Ile His Val Asn His	
210 215 220	
ccc aag gaa atc acc ccc gaa gtg gcc gag gcg tgt gac cgt ctg acc	720
Pro Lys Glu Ile Thr Pro Glu Val Ala Glu Ala Cys Asp Arg Leu Thr	
225 230 235 240	
cgc gcg ggc gtg ccg ctc ggc aac cag agc gtg ctg ctg cgc ggc gtg	768
Arg Ala Gly Val Pro Leu Gly Asn Gln Ser Val Leu Leu Arg Gly Val	
245 250 255	
aac gac cac ccg gtc atc atg caa aag ctg ctg cgc gag ctc gtc aaa	816
Asn Asp His Pro Val Ile Met Gln Lys Leu Leu Arg Glu Leu Val Lys	
260 265 270	
att cgg gtg cgc ccc tac tac atc tac cag tgc gac ctc gtg cac ggc	864
Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Val His Gly	
275 280 285	
gct ggg cac ctg cgc acc acg gtc agt aag ggt ctg gaa atc atg gaa	912
Ala Gly His Leu Arg Thr Thr Val Ser Lys Gly Leu Glu Ile Met Glu	
290 295 300	
tcg ctg cgc ggc cac acc tcc ggc tac agc gtg ccg acc tac gtg gtg	960
Ser Leu Arg Gly His Thr Ser Gly Tyr Ser Val Pro Thr Tyr Val Val	
305 310 315 320	

gac gcg ccc ggc ggc ggc ggc aag att ccg gtg gcg ccc aac tac gtg 1008  
 Asp Ala Pro Gly Gly Gly Gly Lys Ile Pro Val Ala Pro Asn Tyr Val  
                   325                  330                  335

ctc tcg cac agc cct gag aag ctg att ctg cgc aac ttc gag ggc tac 1056  
 Leu Ser His Ser Pro Glu Lys Leu Ile Leu Arg Asn Phe Glu Gly Tyr  
                   340                  345                  350

atc gcc gcc tac tcg gag ccc acc gat tac acc ggc ccc gac atg gcg 1104  
 Ile Ala Ala Tyr Ser Glu Pro Thr Asp Tyr Thr Gly Pro Asp Met Ala  
                   355                  360                  365

att cct gac gac tgg att cgc aag gaa ccc ggc cag acc ggc atc ttc 1152  
 Ile Pro Asp Asp Trp Ile Arg Lys Glu Pro Gly Gln Thr Gly Ile Phe  
                   370                  375                  380

ggc ctg atg gaa ggc gag cgc att tcc atc gag ccg 1188  
 Gly Leu Met Glu Gly Glu Arg Ile Ser Ile Glu Pro  
                   385                  390                  395

<210> 12  
 <211> 396  
 <212> PRT  
 <213> Deinococcus radiodurans

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Lys Asn Arg Ile Asn Ser Val Glu Glu Leu Gln Glu Val Leu Thr Leu  
                   20                  25                  30

Thr Glu Ser Glu Tyr Arg Gly Ala Ser Ala Glu Gly Ile Phe Arg Leu  
                   35                  40                  45

Asp Ile Thr Pro Tyr Phe Ala Ser Leu Met Asp Pro Glu Asp Pro Thr  
                   50                  55                  60

Cys Pro Val Arg Arg Gln Val Ile Pro Thr Glu Glu Glu Leu Gln Pro  
                   65                  70                  75                  80

Phe Thr Ser Met Met Glu Asp Ser Leu Ala Glu Asp Lys His Ser Pro  
                   85                  90                  95

Val Pro Gly Leu Val His Arg Tyr Pro Asp Arg Val Leu Met Leu Val  
                   100                  105                  110

Thr Thr Gln Cys Ala Ser Tyr Cys Arg Tyr Cys Thr Arg Ser Arg Ile  
                   115                  120                  125

Val Gly Asp Pro Thr Glu Thr Phe Asn Pro Ala Glu Tyr Glu Ala Gln  
                   130                  135                  140

Leu Asn Tyr Leu Arg Asn Thr Pro Gln Val Arg Asp Val Leu Leu Ser  
                   145                  150                  155                  160

Gly Gly Asp Pro Leu Thr Leu Ala Pro Lys Val Leu Gly Arg Leu Leu  
                   165                  170                  175

Ser Glu Leu Arg Lys Ile Glu His Ile Glu Ile Ile Arg Ile Gly Thr  
                   180                  185                  190

Arg Val Pro Val Phe Met Pro Met Arg Val Thr Gln Glu Leu Cys Asp  
 195 200 205  
 Thr Leu Ala Glu His His Pro Leu Trp Met Asn Ile His Val Asn His  
 210 215 220  
 Pro Lys Glu Ile Thr Pro Glu Val Ala Glu Ala Cys Asp Arg Leu Thr  
 225 230 235 240  
 Arg Ala Gly Val Pro Leu Gly Asn Gln Ser Val Leu Leu Arg Gly Val  
 245 250 255  
 Asn Asp His Pro Val Ile Met Gln Lys Leu Leu Arg Glu Leu Val Lys  
 260 265 270  
 Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Val His Gly  
 275 280 285  
 Ala Gly His Leu Arg Thr Thr Val Ser Lys Gly Leu Glu Ile Met Glu  
 290 295 300  
 Ser Leu Arg Gly His Thr Ser Gly Tyr Ser Val Pro Thr Tyr Val Val  
 305 310 315 320  
 Asp Ala Pro Gly Gly Gly Lys Ile Pro Val Ala Pro Asn Tyr Val  
 325 330 335  
 Leu Ser His Ser Pro Glu Lys Leu Ile Leu Arg Asn Phe Glu Gly Tyr  
 340 345 350  
 Ile Ala Ala Tyr Ser Glu Pro Thr Asp Tyr Thr Gly Pro Asp Met Ala  
 355 360 365  
 Ile Pro Asp Asp Trp Ile Arg Lys Glu Pro Gly Gln Thr Gly Ile Phe  
 370 375 380  
 Gly Leu Met Glu Gly Glu Arg Ile Ser Ile Glu Pro  
 385 390 395

<210> 13  
 <211> 1113  
 <212> DNA  
 <213> Aquifex aeolicus

<220>  
 <221> CDS  
 <222> (1)..(1110)

<400> 13  
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 Met Arg Arg Phe Phe Glu Asn Val Pro Glu Asn Leu Trp Arg Ser Tyr  
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 gag tgg cag ata caa aac agg ata aaa act ctt aag gag ata aaa aag 96  
 Glu Trp Gln Ile Gln Asn Arg Ile Lys Thr Leu Lys Glu Ile Lys Lys  
 20 25 30  
 tac tta aaa ctc ctt ccc gag gag gaa gaa gga att aaa aga act caa 144  
 Tyr Leu Lys Leu Leu Pro Glu Glu Glu Glu Gly Ile Lys Arg Thr Gln  
 35 40 45

ggg ctt tat ccc ttt gcg ata aca cct tac tac ctc tct tta ata aat	192
Gly Leu Tyr Pro Phe Ala Ile Thr Pro Tyr Tyr Leu Ser Leu Ile Asn	
50 55 60	
cca gag gac ccg aag gat cct ata aga ctt cag gca atc ccc cgc gtt	240
Pro Glu Asp Pro Lys Asp Pro Ile Arg Leu Gln Ala Ile Pro Arg Val	
65 70 75 80	
gta gaa gtt gat gaa aag gtt cag tct gcg gga gaa cca gac gct ctg	288
Val Glu Val Asp Glu Lys Val Gln Ser Ala Gly Glu Pro Asp Ala Leu	
85 90 95	
aaa gaa gaa gga gat att ccg ggt ctt aca cac agg tat ccc gac agg	336
Lys Glu Glu Gly Asp Ile Pro Gly Leu Thr His Arg Tyr Pro Asp Arg	
100 105 110	
gtt ctt tta aac gtc act acc ttt tgt gcg gtt tac tgc agg cac tgt	384
Val Leu Leu Asn Val Thr Thr Phe Cys Ala Val Tyr Cys Arg His Cys	
115 120 125	
atg aga aag agg ata ttc tct cag ggt gag agg gca agg act aaa gag	432
Met Arg Lys Arg Ile Phe Ser Gln Gly Glu Arg Ala Arg Thr Lys Glu	
130 135 140	
gaa ata gac acg atg att gat tac ata aag aga cac gaa gag ata agg	480
Glu Ile Asp Thr Met Ile Asp Tyr Ile Lys Arg His Glu Glu Ile Arg	
145 150 155 160	
gat gtc tta att tca ggt ggt gag cca ctt tcc ctt tcc ttg gaa aaa	528
Asp Val Leu Ile Ser Gly Gly Glu Pro Leu Ser Leu Ser Leu Glu Lys	
165 170 175	
ctt gaa tac tta ctc tca agg tta agg gaa ata aaa cac gtg gaa att	576
Leu Glu Tyr Leu Leu Ser Arg Leu Arg Glu Ile Lys His Val Glu Ile	
180 185 190	
ata cgc ttt ggg acg agg ctt ccc gtt ctt gca ccc cag agg ttc ttt	624
Ile Arg Phe Gly Thr Arg Leu Pro Val Leu Ala Pro Gln Arg Phe Phe	
195 200 205	
aac gat aaa ctt ctg gac ata ctg gaa aaa tac tcc ccc ata tgg ata	672
Asn Asp Lys Leu Leu Asp Ile Leu Glu Lys Tyr Ser Pro Ile Trp Ile	
210 215 220	
aac act cac ttc aac cat ccg aat gag ata acc gag tac gcg gaa gaa	720
Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Tyr Ala Glu Glu	
225 230 235 240	
gcg gtg gac agg ctc ctg aga agg ggc att ccc gtg aac aac cag aca	768
Ala Val Asp Arg Leu Leu Arg Arg Gly Ile Pro Val Asn Asn Gln Thr	
245 250 255	
gtc cta ctt aaa ggc gta aac gac gac cct gaa gtt atg cta aaa ctc	816
Val Leu Leu Lys Gly Val Asn Asp Asp Pro Glu Val Met Leu Lys Leu	
260 265 270	
ttt aga aaa ctt tta agg ata aag gta aag ccc cag tac ctc ttt cac	864
Phe Arg Lys Leu Leu Arg Ile Lys Val Lys Pro Gln Tyr Leu Phe His	
275 280 285	
tgc gac ccg ata aag gga gcg gtt cac ttt agg act acg ata gac aaa	912
Cys Asp Pro Ile Lys Gly Ala Val His Phe Arg Thr Thr Ile Asp Lys	
290 295 300	

gga ctt gaa ata atg aga tat ttg agg gga agg ctg agc ggt ttc ggg 960  
 Gly Leu Glu Ile Met Arg Tyr Leu Arg Gly Arg Leu Ser Gly Phe Gly  
 305 310 315 320  
 ata ccc act tac gcg gtg gac ctc ccg gga ggg aaa ggt aag gtt cct 1008  
 Ile Pro Thr Tyr Ala Val Asp Leu Pro Gly Gly Lys Gly Lys Val Pro  
 325 330 335  
 ctt ctt ccc aac tac gta aag aaa agg aaa ggt aat aag ttc tgg ttt 1056  
 Leu Leu Pro Asn Tyr Val Lys Lys Arg Lys Gly Asn Lys Phe Trp Phe  
 340 345 350  
 gaa agt ttc acg ggt gag gtc gta gaa tac gaa gta acg gaa gta tgg 1104  
 Glu Ser Phe Thr Gly Glu Val Val Glu Tyr Glu Val Thr Glu Val Trp  
 355 360 365  
 gaa cct tga 1113  
 Glu Pro  
 370

<210> 14  
 <211> 370  
 <212> PRT  
 <213> Aquifex aeolicus

<400> 14  
 Met Arg Arg Phe Phe Glu Asn Val Pro Glu Asn Leu Trp Arg Ser Tyr  
 1 5 10 15  
 Glu Trp Gln Ile Gln Asn Arg Ile Lys Thr Leu Lys Glu Ile Lys Lys  
 20 25 30  
 Tyr Leu Lys Leu Leu Pro Glu Glu Glu Glu Gly Ile Lys Arg Thr Gln  
 35 40 45  
 Gly Leu Tyr Pro Phe Ala Ile Thr Pro Tyr Tyr Leu Ser Leu Ile Asn  
 50 55 60  
 Pro Glu Asp Pro Lys Asp Pro Ile Arg Leu Gln Ala Ile Pro Arg Val  
 65 70 75 80  
 Val Glu Val Asp Glu Lys Val Gln Ser Ala Gly Glu Pro Asp Ala Leu  
 85 90 95  
 Lys Glu Glu Gly Asp Ile Pro Gly Leu Thr His Arg Tyr Pro Asp Arg  
 100 105 110  
 Val Leu Leu Asn Val Thr Thr Phe Cys Ala Val Tyr Cys Arg His Cys  
 115 120 125  
 Met Arg Lys Arg Ile Phe Ser Gln Gly Glu Arg Ala Arg Thr Lys Glu  
 130 135 140  
 Glu Ile Asp Thr Met Ile Asp Tyr Ile Lys Arg His Glu Glu Ile Arg  
 145 150 155 160  
 Asp Val Leu Ile Ser Gly Gly Glu Pro Leu Ser Leu Ser Leu Glu Lys  
 165 170 175  
 Leu Glu Tyr Leu Leu Ser Arg Leu Arg Glu Ile Lys His Val Glu Ile  
 180 185 190

Ile Arg Phe Gly Thr Arg Leu Pro Val Leu Ala Pro Gln Arg Phe Phe  
 195 200 205  
 Asn Asp Lys Leu Leu Asp Ile Leu Glu Lys Tyr Ser Pro Ile Trp Ile  
 210 215 220  
 Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Tyr Ala Glu Glu  
 225 230 235 240  
 Ala Val Asp Arg Leu Leu Arg Arg Gly Ile Pro Val Asn Asn Gln Thr  
 245 250 255  
 Val Leu Leu Lys Gly Val Asn Asp Asp Pro Glu Val Met Leu Lys Leu  
 260 265 270  
 Phe Arg Lys Leu Leu Arg Ile Lys Val Lys Pro Gln Tyr Leu Phe His  
 275 280 285  
 Cys Asp Pro Ile Lys Gly Ala Val His Phe Arg Thr Thr Ile Asp Lys  
 290 295 300  
 Gly Leu Glu Ile Met Arg Tyr Leu Arg Gly Arg Leu Ser Gly Phe Gly  
 305 310 315 320  
 Ile Pro Thr Tyr Ala Val Asp Leu Pro Gly Gly Lys Gly Lys Val Pro  
 325 330 335  
 Leu Leu Pro Asn Tyr Val Lys Lys Arg Lys Gly Asn Lys Phe Trp Phe  
 340 345 350  
 Glu Ser Phe Thr Gly Glu Val Val Glu Tyr Glu Val Thr Glu Val Trp  
 355 360 365  
 Glu Pro  
 370

<210> 15  
 <211> 1065  
 <212> DNA  
 <213> *Treponema pallidum*

<220>  
 <221> CDS  
 <222> (1)..(1065)

<400> 15  
 atg tct atg gct gag tgt acc cgg gaa cag aga aag aga cga ggt gca 48  
 Met Ser Met Ala Glu Cys Thr Arg Glu Gln Arg Lys Arg Arg Gly Ala  
 1 5 10 15  
 ggg cgt gct gat gag cat tgg cgg acg ttg agt cct gcc tct tgc gcg 96  
 Gly Arg Ala Asp Glu His Trp Arg Thr Leu Ser Pro Ala Ser Cys Ala  
 20 25 30  
 gca gat gcg ctg acg gag cat att tct cca gcg tat gcg cat tta att 144  
 Ala Asp Ala Leu Thr Glu His Ile Ser Pro Ala Tyr Ala His Leu Ile  
 35 40 45  
 gca caa gcg cag ggc gcg gac gcg cag gcg ctg aaa cgt cag gtg tgc 192  
 Ala Gln Ala Gln Gly Ala Asp Ala Gln Ala Leu Lys Arg Gln Val Cys  
 50 55 60

ttt gcg cca cag gag cgt gtg gtg cat gct tgc gag tgt gcc gac cca	240
Phe Ala Pro Gln Glu Arg Val Val His Ala Cys Glu Cys Ala Asp Pro	
65 70 75 80	
ttg ggt gag gac cgg tac tgc gtg aca ccc ttt ttg gtg cat cag tat	288
Leu Gly Glu Asp Arg Tyr Cys Val Thr Pro Phe Leu Val His Gln Tyr	
85 90 95	
gcg aat cgt gtg ttg atg ttg gca aca gga cgt tgc ttt tca cac tgt	336
Ala Asn Arg Val Leu Met Leu Ala Thr Gly Arg Cys Phe Ser His Cys	
100 105 110	
cgc tat tgt ttt cgc cgc ggt ttc atc gcc caa cgt gca ggg tgg atc	384
Arg Tyr Cys Phe Arg Arg Gly Phe Ile Ala Gln Arg Ala Gly Trp Ile	
115 120 125	
ccc aac gaa gag cgc gag aag att att acg tat ctt cgt gct acc cct	432
Pro Asn Glu Glu Arg Glu Lys Ile Ile Thr Tyr Leu Arg Ala Thr Pro	
130 135 140	
tcg gtg aag gaa atc ctg gtt tca ggt ggt gat cca ctc act ggt tct	480
Ser Val Lys Glu Ile Leu Val Ser Gly Gly Asp Pro Leu Thr Gly Ser	
145 150 155 160	
ttt gca cag gtc aca tcg ctt ttc cgc gca ctg cgc agt gta gcg ccg	528
Phe Ala Gln Val Thr Ser Leu Phe Arg Ala Leu Arg Ser Val Ala Pro	
165 170 175	
gat ttg att att cgt ctg tgc act cgc gca gtc acc ttt gct ccg cag	576
Asp Leu Ile Ile Arg Leu Cys Thr Arg Ala Val Thr Phe Ala Pro Gln	
180 185 190	
gcc ttt act ccc gag ctg att gcg ttt ctg cag gag atg aag ccg gtg	624
Ala Phe Thr Pro Glu Leu Ile Ala Phe Leu Gln Glu Met Lys Pro Val	
195 200 205	
tggtg ata att ccg cat att aat cac ccg gca gag ctc ggt tct acg cag	672
Trp Ile Ile Pro His Ile Asn His Pro Ala Glu Leu Gly Ser Thr Gln	
210 215 220	
cgc gcg gtg ctc gag gcc tgc gta ggc gca ggc ctc cct gtg caa tcg	720
Arg Ala Val Leu Glu Ala Cys Val Gly Ala Gly Leu Pro Val Gln Ser	
225 230 235 240	
cag tcg gta ctg ttg cgc ggg gtg aac gat tcg gta gag acg ctg tgc	768
Gln Ser Val Leu Leu Arg Gly Val Asn Asp Ser Val Glu Thr Leu Cys	
245 250 255	
aca ctg ttt cac gcg ctc act tgt ctg ggg gtt aag ccg ggg tat cta	816
Thr Leu Phe His Ala Leu Thr Cys Leu Gly Val Lys Pro Gly Tyr Leu	
260 265 270	
ttt cag ttg gat ttg gcg cct gga act ggg gat ttt cgt gtg cca ctt	864
Phe Gln Leu Asp Leu Ala Pro Gly Thr Gly Asp Phe Arg Val Pro Leu	
275 280 285	
tct gac acg cta gct ctg tgg cgc aca ttg aag gag cgc ctc tca ggg	912
Ser Asp Thr Leu Ala Leu Trp Arg Thr Leu Lys Glu Arg Leu Ser Gly	
290 295 300	
ttg tcg ctt ccc acg ctt gcg gtg gac ttg cca ggg ggt gga gga aag	960
Leu Ser Leu Pro Thr Leu Ala Val Asp Leu Pro Gly Gly Gly Gly Lys	
305 310 315 320	

ttt ccg ctt gtg gca ttg gcc ttg cag caa gat gtc acg tgg cat cag 1008  
 Phe Pro Leu Val Ala Leu Ala Leu Gln Gln Asp Val Thr Trp His Gln  
 325 330 335  
  
 gaa cgc gag gcg ttc tcc gca cgc ggc atc gat ggc gcg tgg tac acg 1056  
 Glu Arg Glu Ala Phe Ser Ala Arg Gly Ile Asp Gly Ala Trp Tyr Thr  
 340 345 350  
  
 tac ccg ttc 1065  
 Tyr Pro Phe  
 355

<210> 16  
 <211> 355  
 <212> PRT  
 <213> Treponema pallidum

<400> 16  
 Met Ser Met Ala Glu Cys Thr Arg Glu Gln Arg Lys Arg Arg Gly Ala  
 1 5 10 15  
 Gly Arg Ala Asp Glu His Trp Arg Thr Leu Ser Pro Ala Ser Cys Ala  
 20 25 30  
 Ala Asp Ala Leu Thr Glu His Ile Ser Pro Ala Tyr Ala His Leu Ile  
 35 40 45  
 Ala Gln Ala Gln Gly Ala Asp Ala Gln Ala Leu Lys Arg Gln Val Cys  
 50 55 60  
 Phe Ala Pro Gln Glu Arg Val Val His Ala Cys Glu Cys Ala Asp Pro  
 65 70 75 80  
 Leu Gly Glu Asp Arg Tyr Cys Val Thr Pro Phe Leu Val His Gln Tyr  
 85 90 95  
 Ala Asn Arg Val Leu Met Leu Ala Thr Gly Arg Cys Phe Ser His Cys  
 100 105 110  
 Arg Tyr Cys Phe Arg Arg Gly Phe Ile Ala Gln Arg Ala Gly Trp Ile  
 115 120 125  
 Pro Asn Glu Glu Arg Glu Lys Ile Ile Thr Tyr Leu Arg Ala Thr Pro  
 130 135 140  
 Ser Val Lys Glu Ile Leu Val Ser Gly Gly Asp Pro Leu Thr Gly Ser  
 145 150 155 160  
 Phe Ala Gln Val Thr Ser Leu Phe Arg Ala Leu Arg Ser Val Ala Pro  
 165 170 175  
 Asp Leu Ile Ile Arg Leu Cys Thr Arg Ala Val Thr Phe Ala Pro Gln  
 180 185 190  
 Ala Phe Thr Pro Glu Leu Ile Ala Phe Leu Gln Glu Met Lys Pro Val  
 195 200 205  
 Trp Ile Ile Pro His Ile Asn His Pro Ala Glu Leu Gly Ser Thr Gln  
 210 215 220  
 Arg Ala Val Leu Glu Ala Cys Val Gly Ala Gly Leu Pro Val Gln Ser  
 225 230 235 240



Gln Ser Val Leu Leu Arg Gly Val Asn Asp Ser Val Glu Thr Leu Cys  
                   245                                  250                                  255  
 Thr Leu Phe His Ala Leu Thr Cys Leu Gly Val Lys Pro Gly Tyr Leu  
                   260                                  265                                  270  
 Phe Gln Leu Asp Leu Ala Pro Gly Thr Gly Asp Phe Arg Val Pro Leu  
                   275                                  280                                  285  
 Ser Asp Thr Leu Ala Leu Trp Arg Thr Leu Lys Glu Arg Leu Ser Gly  
                   290                                  295                                  300  
 Leu Ser Leu Pro Thr Leu Ala Val Asp Leu Pro Gly Gly Gly Gly Lys  
                   305                                  310                                  315                                  320  
 Phe Pro Leu Val Ala Leu Ala Leu Gln Gln Asp Val Thr Trp His Gln  
                   325                                  330                                  335  
 Glu Arg Glu Ala Phe Ser Ala Arg Gly Ile Asp Gly Ala Trp Tyr Thr  
                   340                                  345                                  350  
 Tyr Pro Phe  
                   355

<210> 17  
 <211> 6  
 <212> PRT  
 <213> Clostridium subterminale

<400> 17  
 Lys Asp Val Ser Asp Ala  
   1                                  5

<210> 18  
 <211> 17  
 <212> DNA  
 <213> Clostridium subterminale

<220>  
 <221> modified\_base  
 <222> (9)  
 <223> n is inosine

<220>  
 <221> modified\_base  
 <222> (12)  
 <223> n is inosine

<400> 18  
 aargaygtmw sngaygc

17

<210> 19  
 <211> 6  
 <212> PRT  
 <213> Clostridium subterminale

<400> 19  
 Gln Ser His Asp Lys Val  
   1                                  5

<210> 20  
<211> 20  
<212> DNA  
<213> Clostridium subterminale

<220>  
<221> modified\_base  
<222> (3)  
<223> n is inosine

<220>  
<221> modified\_base  
<222> (15)  
<223> n is inosine

<400> 20  
atnacytttrt crtgnswytg

20

<210> 21  
<211> 48  
<212> PRT  
<213> Clostridium subterminale

<400> 21  
Pro Asn Tyr Val Ile Ser Gln Ser His Asp Lys Val Ile Leu Arg Asn  
1 5 10 15

Phe Glu Gly Val Ile Thr Thr Tyr Ser Glu Pro Ile Asn Tyr Thr Pro  
20 25 30

Gly Cys Asn Cys Asp Val Cys Thr Gly Lys Lys Lys Val His Lys Val  
35 40 45

<210> 22  
<211> 15  
<212> PRT  
<213> Clostridium subterminale

<400> 22  
Ala Leu Glu Pro Val Gly Leu Glu Arg Asn Lys Arg His Val Gln  
1 5 10 15

<210> 23  
<211> 16  
<212> PRT  
<213> Clostridium subterminale

<400> 23  
Met Ile Asn Arg Arg Tyr Glu Leu Phe Lys Asp Val Ser Asp Ala Asp  
1 5 10 15

<210> 24  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 24  
atcctaacga tcctaatagat cc 22

<210> 25  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 25  
tggatgggta aagtgaagtg 19

<210> 26  
<211> 500  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Probe

<400> 26  
atcctaacga tcctaatagat ccagtaagaa aacaagctat tccaacagca ttagagctta 60  
acaaagctgc tgcagatctt gaagacccat tacatgaaga tacagattca ccagtacctg 120  
gattaactca cagatatcca gatagagtat tattattaat aactgatatg tgctcaatgt 180  
actgcagaca ctgtacaaga agaagatttg caggacaaag cgatgactct atgccaatgg 240  
aaagaataga taaagctata gattatatca gaaatactcc tcaagttaga gacgtattat 300  
tatcaggtgg agacgctctt ttagtatctg atgaaacatt agaatacatc atagctaaat 360  
taagagaaat accacacgtt gaaatagtaa gaatagggttc aagaactcca gttgttcttc 420  
caciaaagaat aactccagaa cttgtaaata tgcttaaaaa atatcatcca gtatgggttaa 480  
acactcactt taaccatcca 500

<210> 27  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 27  
tacacatatg ataaatagaa gatatg 26

<210> 28  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 28

tagactcgag ttattcttga acgtgtctc

29

<210> 29

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 29

tacagaattc atgataaata gaagatatg

29

<210> 30

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 30

tagaaagctt ttattcttga acgtgtctc

29

<210> 31

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 31

tataggatcc gaccgtataa ttcacgcgat tacacc

36

<210> 32

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 32

tagagaattc gattcagtc ggcgtcccat tatc

34